

PATENT

Atty. Docket No. PP1641.102

readable format is the same as the paper sequence listing. Also accompanying this amendment is a diskette with the computer readable format.

Applicants respectfully submit that the application is now in condition for examination, and solicit such action at an early date. If there are any questions that could be resolved by a telephone interview, the Examiner is invited to telephone the undersigned at the number below.

Respectfully submitted,

Dated:

Feb 22, 2002

By:

Rebecca M. Hale

Rebecca M. Hale

Reg. No. 45,680

CHIRON CORPORATION

Intellectual Property - R440

P.O. Box 8097

Emeryville, CA 94608

(510) 923-3179

(510) 655-3542 (Fax)

**TABLE III – N-TERMINAL SEQUENCES OF PROTEINS**

Spot #	N-terminal sequence
10	SKETFQRNK (SEQ ID NO. 1)
12	TTESLETLVE (SEQ. ID NO. 2)
15	LAVSSGDQEVSQEDLLKE (SEQ. ID NO. 3)
18	XPAGNPAFPVIP (SEQ. ID NO. 4)
21	AKTRTLKGDG (SEQ ID NO. 5)
24	SDSSHNLLYNK (SEQ ID NO. 6)
25	VLLYSQASWDQRSKADAL (SEQ. ID NO. 7)
26	KAVYVQD(A/Q)E(V/D)Q (SEQ. ID NO. 8)
31	KDxxTNGQR (SEQ ID NO. 9)
33	MSKGGQtxD(Y/G) (SEQ. ID NO. 10)
38	XQXENGIVGL (SEQ. ID NO. 11)
46	MPAGNPAFPVIP (SEQ. ID NO. 12)

**TABLE IV – IDENTIFICATION OF ANTIGENS**

“CT-D gene” refers to the gene name from reference 2 and gives the names of genes likely to encode homologue proteins in *C.trachomatis* D. Theoretical pI/MW values in the last column, to be compared to the experimental values, were calculated the from CT-D gene sequences.

spot	Map location	N-terminal AA seq	Annotation	CT-D gene	Predicted pI/MW
1	OMP2 cluster	-	OMP2	<i>omcB</i>	7.65-7.92/54.5-58.7
2	5.2-5.3/59.7	VA(D/K)NI(K/F)YNEE (SEQ ID NO. 13)	GroEL-like	<i>groEL1</i>	5.11/58.1
3	4.6-4.9/40	LPVGN (SEQ ID NO. 14)	MOMP	<i>ompA</i>	4.69/40.3
4	4.92-5.04/70.5	SEKRK(S/A)N(K/S). (SEQ ID NO. 15)	DnaK-like	<i>dnaK</i>	4.88/70.7
10	5.44-5.64/42.2	SKETFQRNK (SEQ ID NO. 1)	EF-Tu	<i>tufA</i>	5.36/43.1
12	4.80/15.8	TTESLETLVE (SEQ ID NO. 2)	Ribosomal protein L7/12	<i>rfl7</i>	5.09/13.5
15	5.89/48.4	LAVSSGDQEVSQEDLLKE (SEQ ID NO. 3)	stress induced protease	<i>htrA</i>	5.83/49.5
18	5.08/34.09	XPAGNPAFPVIP (SEQ ID NO. 4)	outer membrane protein	<i>ompB</i>	5.06/34.5
19	5.14-5.28/69	Not determined	Ribosomal protein S1	<i>rs1</i>	5.17/63.6
21	5.27/40.5	AKTRTLKGDG (SEQ ID NO. 5)	EF-Tu related peptide?	-	-
24	5.32/40.5	SDSSHNLLYNK (SEQ ID NO. 6)	RNAP alpha chain	<i>rpoA</i>	5.34/41.7
25	5.97/47.6	VLLYSQASWDQRSKADAL (SEQ ID NO. 7)	Aminopeptidase	<i>pepA</i>	5.74/54.0
26	5.68/48.6	KAVYVQD(A/Q)E(V/D)Q (SEQ ID NO. 8)	Not identified	-	-
31	5.43/40.4	KDxxTNGQR (SEQ ID NO. 9)	Not identified	-	-
33	6.64/25.4	MSKGGQtxD(Y/G) (SEQ ID NO. 10)	Not identified	-	-
38	5.23/40.1	XQXENGIVGL (SEQ ID NO. 11)	GTP-binding protein	<i>ychF</i>	5.16/39.5
46	5.19/33.4	MPAGNPAFPVIP (SEQ ID NO. 12)	outer membrane protein	<i>ompB</i>	5.06/34.5